AMENDMENTS

Amendments to the Claims:

Please cancel claims 16-48 without prejudice or disclaimer and please amend claim 1 as set forth in the complete listing of the claims below. The listing hereafter replaces all prior versions and listings.

1 (currently amended). A method for identifying a subject at risk of melanoma, which comprises detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of

(a) the nucleotide sequence of SEQ ID NO: 1;

(b) a nucleotide sequence which encodes an amino acid sequence encoded by SEQ ID NO: 1 ~~a polypeptide consisting of the amino acid sequence set forth in Figures 2A to 2G or Figure 3B~~;

(c) a nucleotide sequence which encodes an amino acid sequence that is 90% or more identical to the amino acid sequence encoded by SEQ ID NO: 1 ~~a polypeptide that is 90% or more identical to the amino acid sequence set forth in Figures 2A to 2G or Figure 3B~~;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

wherein the nucleotide sequence contains a thymine at position 171429 of SEQ ID NO: 1 ~~polymorphic variation does not alter the valine at position 599 in the amino acid sequence set forth in Figure 3B~~;

whereby the presence of the polymorphic variation is indicative of the subject being at risk of melanoma.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (original). The method of claim 1, wherein the polymorphic variations is detected at position the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 146311, 138875, 132526, 128002, 118712, 98846, 98682, 87826, 80400, 76779, 68398 and 64547.

4 (original). The method of claim 3, wherein a polymorphic variation is detected at position 146311 in SEQ ID NO:1.

5 (original). The method of claim 3, wherein a polymorphic variation is detected at position 132526 in SEQ ID NO:1.

6 (original). The method of claim 3, wherein a polymorphic variation is detected at position 128002 in SEQ ID NO:1.

7 (original). The method of claim 3, wherein a polymorphic variation is detected at position 118712 in SEQ ID NO:1.

8 (original). The method of claim 3, wherein a polymorphic variation is detected at position 98846 in SEQ ID NO:1.

9 (original). The method of claim 3, wherein a polymorphic variation is detected at position 80400 in SEQ ID NO:1.

10 (original). The method of claim 3, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in SEQ ID NO: 1 selected from the group consisting of 146311, 138875, 132526, 128002, 118712, 98846, 98682, 87826, 80400, 76779, 68398 and 64547.

11 (original). The method of claim 3, wherein the polymorphic variation is the haplotype CTTG corresponding to positions 146311, 138875, 76779, and 68398, respectively, in SEQ ID NO: 1.

12 (original). The method of claim 3, wherein the polymorphic variation is the haplotype ATGA corresponding to positions 146311, 138875, 76779, and 68398, respectively, in SEQ ID NO: 1.

13 (original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

14 (previously presented). The method of claim 13, wherein the oligonucleotide is selected from the group consisting of GTAATGTTGAAACTACAATTACCA (SEQ ID NO: 45); GAAACAGGCTTCAATTCATCTT (SEQ ID NO: 46); ACATAGAGGCAGGACTGTCA (SEQ ID NO: 47); ATTAGGACATGGCTGAGATATTCA (SEQ ID NO: 48); GGACTCTGCTTATTCTACCCA (SEQ ID NO: 49); AGAGATTGTGCTTCCCAAATC (SEQ ID NO: 50); GAATTAGTGAACTCTGGAAAGT (SEQ ID NO: 51); GAAATATGTTTGGAAAATTGTTCT (SEQ ID NO: 52); CTACAAAGCAAGACAGGACTAA (SEQ ID NO: 53); CCAAGATAAGAATCTGTTTTACC (SEQ ID NO: 54); AATGTTCTGAATTTTTCCAACTAA (SEQ ID NO: 55); and TTATAATTTAGTGGGGAACAGAA (SEQ ID NO: 56).

15 (original). The method of claim 1, wherein the subject is a human.

16-48 (cancelled).